

**AMENDMENTS TO THE CLAIMS:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

Claims 1 – 171 (cancelled)

Claim 172 (currently amended) A method of feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase consisting essentially of the amino acid sequence set forth in ~~wherein said desaturase has an amino acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NO:9, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or a subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of all or a part of the isolated nucleic acid fragment either the fragment or subsequence,~~ operably linked to at least one regulatory sequence;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase consisting essentially of the amino acid sequence set forth in ~~wherein said desaturase has an amino acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NO:9, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or a subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of all or a part of the isolated nucleic acid sequence either the fragment or subsequence,~~ and (b) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, wherein the isolated nucleic acid fragments of (a) and (b) are operably linked;

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase consisting essentially of the amino acid sequence set forth in ~~wherein said desaturase has an amino acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NO:9, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or a subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of all or a part of the isolated nucleic acid fragment either the fragment or subsequence,~~ and (b) a shrunken 1 intron/exon, wherein the isolated nucleic acid fragments of (a) and (b) are operably linked to at least one regulatory sequence; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase consisting essentially of the amino acid sequence set forth in ~~wherein said desaturase has an amino acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NO:9, or a subsequence of SEQ ID NO:9, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of all or a part of the isolated nucleic acid fragment either the fragment or subsequence,~~ (b) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the amino acid sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (c) a shrunken 1 ~~intron/exon; intron/exon~~, wherein (a), (b) and (c) are operably linked;

and further wherein expression of the chimeric gene results in an altered corn stearic acid phenotype.

Claims 173 (currently amended) A method feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase, or a subsequence of SEQ ID NO:1 having at

~~least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or part of either the fragment or subsequence, operably linked to at least one regulatory sequence;~~

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase or a subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of either the fragment or subsequence and (b) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49 wherein the isolated nucleic acid fragments of (a) and (b) are operably linked;

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase or a subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of either the fragment or subsequence, and (b) a shrunken 1 intron/exon, wherein the isolated nucleic acid fragments of (a) and (b) are operably linked to at least one regulatory sequence; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase or a, subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of either the fragment or subsequence, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the nucleotide sequence

set forth in any of SEQ ID NOS: 38-40 and 42-49, and (c) a shrunken 1 ~~intron/exon;~~  
intron/exon, wherein (a), (b) and (c) are operably linked;

and further wherein expression of the chimeric gene results in an altered corn oleic acid phenotype.

Claim 174 (currently amended) A method of feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of:

(i) a first chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase consisting essentially of the amino acid sequence set forth in ~~wherein said desaturase has an amino acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NO:9, or a subsequence of SEQ ID NO:9 wherein all or a part of the first isolated nucleic acid is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of~~ all or a part of either the first fragment or subsequence, and linked to a second chimeric gene comprising an a second isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said second fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated second nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase or a subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of either the second fragment or subsequence, operably linked to at least one regulatory sequence;

(ii) a chimeric gene comprising (a) a first isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase consisting essentially of the amino acid sequence set forth in ~~wherein said desaturase has an amino acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NO:9, or a subsequence of SEQ ID NO:9 wherein all or a part of the isolated first nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of~~ all or a part of either the first fragment or subsequence, (b) a second

isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said second fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated second nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase or a subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of either the second fragment or subsequence, and (c) a third isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49 wherein the isolated nucleic acid fragments of (a), (b) and (c) are operably linked;

(iii) a chimeric gene comprising (a) a first isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase consisting essentially of the amino acid sequence set forth in ~~wherein said desaturase has an amino acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NO:9, or a subsequence of SEQ ID NO:9 wherein all or a part of the isolated first nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearyl ACP desaturase~~, or the complement of all or a part of either the first fragment or subsequence, (b) a second isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said second fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated second nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase or a subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of either the second fragment or subsequence, and (c) a shrunken 1 intron/exon, operably linked to at least one regulatory sequence wherein (a), (b) and (c) are operably linked; or

(iv) a chimeric gene comprising (a) a first isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase consisting essentially of the amino acid sequence set forth in ~~wherein said desaturase has an amino acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NO:9, or the complement thereof~~, (b) a second isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein

said second fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, or the complement thereof, (c) a third isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (d) a shrunken 1 intron/exon wherein (a), (b), (c) and (d) are operably linked;

and further wherein expression of the chimeric gene results in an altered corn oil phenotype.

Claim 175 (cancelled)

Claim 176 (currently amended) A method feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of :

(i) a first chimeric gene selected from the group consisting of:

(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase consisting essentially of the amino acid sequence set forth in ~~wherein said desaturase has an amino acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NO:9, wherein the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase or a subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of all or part of either the fragment or subsequence, operably linked to at least one regulatory sequence ;~~

(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase consisting essentially of the nucleotide sequence set forth in ~~wherein said desaturase has an amino acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NO:9, or a subsequence of SEQ ID NO:9 wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of all or a part of either the fragment or subsequence, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting~~

essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49 wherein the isolated nucleic acid fragments of (1) and (2) are operably linked;

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase consisting essentially of the amino acid sequence set forth in ~~wherein said desaturase has an amino acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NO:9, or a subsequence of SEQ ID NO:9~~ wherein all or part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of all or part of either the fragment or subsequence, and (b) (2) a shrunken 1 intron/exon, operably linked to at least one regulatory sequence, wherein the isolated nucleic acid fragments of (1) and (2) are operably linked; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase consisting essentially of the amino acid sequence set forth in ~~wherein said desaturase has an amino acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NO:9, or a subsequence of SEQ ID NO:9~~ wherein all or part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of all or a part of either the fragment or subsequence, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (c) (3) a shrunken 1 intron/exon wherein (1), (2) and (3) are operably linked, and

(ii) a second chimeric gene selected from the set consisting of:

(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase or a subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of either the fragment or subsequence, operably linked to at least one regulatory sequence;

(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase or a subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of either the fragment or subsequence, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49 wherein the isolated nucleic acid fragments of (1) and (2) are operably linked;

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of either the fragment or subsequence, and (2) a shrunken 1 intron/exon, operably linked to at least one regulatory sequence, wherein the isolated nucleic acid fragments of (1) and (2) are operably linked; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase or a subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of either the fragment or subsequence, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (e) (3) a shrunken 1 intron/exon, wherein (1), (2) and (3) are operably linked;

and further wherein expression of the chimeric genes results in an altered corn oil phenotype.

Claim 177 (new) A method feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or part of the fragment, operably linked to at least one regulatory sequence;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of the fragment and (b) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49 wherein the isolated nucleic acid fragments of (a) and (b) are operably linked;

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of the fragment, and (b) a shrunken 1 intron/exon, wherein the isolated nucleic acid fragments of (a) and (b) are operably linked to at least one regulatory sequence; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of the fragment, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (c) a shrunken 1 intron/exon, wherein (a), (b) and (c) are operably linked;

wherein expression of the chimeric gene results in an altered corn oleic acid phenotype, and

further wherein the corn grain has an oil content in the range from about 6% to about 10% on a dry matter basis and further wherein said oil is comprised of not less than 60% oleic acid of the total oil content of the seed.